

SEQUENCE LISTING

<110> Virax Development Pty Ltd

<120> A viral vector and methods of using same

<130> 12521330/JEH

<150> AU 2003905642

<151> 2003-10-15

<150> AU 2003905683

<151> 2003-10-16

<160> 7

<170> PatentIn version 3.1

<210> 1

<211> 1329

<212> .DNA

<213> Human immunodeficiency virus

<220>

<221> CDS

<222> (1)..(1329)

<223>

<400> 1

atg ggt gcg aga gcg tcg gta tta agc ggg gga gaa tta gat aaa tgg	48
Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp	
1 5 10 15	
gaa aaa att cgg tta agg cca ggg gga aag aaa aaa tat aag tta aaa	96
Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys	
20 25 30	
cat ata gta tgg gca agc agg gag cta gaa cga ttc gca gtc aat cct	144
His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro	
35 40 45	
ggc ctg tta gaa aca tca gaa ggc tgc aga caa ata ttg gga cag cta	192
Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu	
50 55 60	
cag cca tcc ctt cag aca gga tca gaa gaa ctt aga tca tta tat aat	240
Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn	
65 70 75 80	
aca gta gca acc ctc tat tgt gta cat caa agg ata gat gta aaa gac	288
Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp	
85 90 95	
acc aag gaa gct tta gag aag ata gag gaa gag caa aac aaa agt aag	336
Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys	
100 105 110	

aaa aag gca cag caa gca gca gct	gca gct ggc aca gga aac agc agc	384
Lys Lys Ala Gln Gln Ala Ala Ala	Ala Ala Gly Thr Gly Asn Ser Ser	
115	125	
cag gtc agc caa aat tac cct ata	gtg cag aac cta cag ggg caa atg	432
Gln Val Ser Gln Asn Tyr Pro Ile	Val Gln Asn Leu Gln Gly Gln Met	
130	140	
gta cat cag gcc ata tca cct aga	act tta aat gca tgg gta aaa gta	480
Val His Gln Ala Ile Ser Pro Arg	Thr Leu Asn Ala Trp Val Lys Val	
145	155	160
gta gaa gaa aag gct ttc agc cca	gaa gta ata ccc atg ttt tca gca	528
Val Glu Glu Lys Ala Phe Ser Pro	Glu Val Ile Pro Met Phe Ser Ala	
165	170	175
tta tca gaa gga gcc acc cca caa	gat tta aac acc atg cta aac aca	576
Leu Ser Glu Gly Ala Thr Pro Gln	Asp Leu Asn Thr Met Leu Asn Thr	
180	185	190
gtg ggg gga cat caa gca gcc atg	caa atg tta aaa gag act atc aat	624
Val Gly Gly His Gln Ala Ala Met	Gln Met Leu Lys Glu Thr Ile Asn	
195	200	205
gag gaa gct gca gaa tgg gat aga	gtg cat cca gtg cat gca ggg cct	672
Glu Glu Ala Ala Glu Trp Asp Arg	Val His Pro Val His Ala Gly Pro	
210	215	220
att gca cca ggc caa atg aga gaa	cca agg gga agt gac ata gca gga	720
Ile Ala Pro Gly Gln Met Arg Glu	Pro Arg Gly Ser Asp Ile Ala Gly	
225	230	235
act act agt acc ctt cag gaa caa	ata gga tgg atg aca aat aat cca	768
Thr Thr Ser Thr Leu Gln Glu Gln	Ile Gly Trp Met Thr Asn Asn Pro	
245	250	255
cct atc cca gta gga gaa atc tat	aaa aga tgg ata atc ctg gga tta	816
Pro Ile Pro Val Gly Glu Ile Tyr	Lys Arg Trp Ile Ile Leu Gly Leu	
260	265	270
aat aaa ata gta aga atg tat agc	cct acc agc att ctg gac ata aga	864
Asn Lys Ile Val Arg Met Tyr Ser	Pro Thr Ser Ile Leu Asp Ile Arg	
275	280	285
caa gga cca aag gaa ccc ttt aga	gat tat gta gac cgg ttc tat aaa	912
Gln Gly Pro Lys Glu Pro Phe Arg	Asp Tyr Val Asp Arg Phe Tyr Lys	
290	295	300
act cta aga gcc gaa caa gct tca	cag gat gta aaa aat tgg atg aca	960
Thr Leu Arg Ala Glu Gln Ala Ser	Gln Asp Val Lys Asn Trp Met Thr	
305	310	315
gaa acc ttg ttg gtc caa aat gca	aac cca gat tgt aag act att tta	1008
Glu Thr Leu Leu Val Gln Asn Ala	Asn Pro Asp Cys Lys Thr Ile Leu	
325	330	335

aaa gca ttg gga cca gca gct aca cta gaa gaa atg atg aca gca tgt 1056
 Lys Ala Leu Gly Pro Ala Ala Thr Leu Glu Glu Met Met Thr Ala Cys
 340 345 350

cag gga gtg ggg gga ccc ggc cat aaa gca aga gtt ttg gct gaa gcc 1104
 Gln Gly Val Gly Gly Pro Gly His Lys Ala Arg Val Leu Ala Glu Ala
 355 360 365

atg agc caa gta aca aat cca gct aac ata atg atg cag aga ggc aat 1152
 Met Ser Gln Val Thr Asn Pro Ala Asn Ile Met Met Gln Arg Gly Asn
 370 375 380

ttt agg aac caa aga aag act gtt aag tgt ttc aat tgt ggc aaa gaa 1200
 Phe Arg Asn Gln Arg Lys Thr Val Lys Cys Phe Asn Cys Gly Lys Glu
 385 390 395 400

ggg cac ata gcc aaa aat tgc agg gcc cct agg aaa aag ggc tgt tgg 1248
 Gly His Ile Ala Lys Asn Cys Arg Ala Pro Arg Lys Lys Gly Cys Trp
 405 410 415

aga tgt gga agg gaa gga cac caa atg aaa gat tgc act gag aga cag 1296
 Arg Cys Gly Arg Glu Gly His Gln Met Lys Asp Cys Thr Glu Arg Gln
 420 425 430

gct aat ttt tta ggg aag atc tgg cct tcc tac 1329
 Ala Asn Phe Leu Gly Lys Ile Trp Pro Ser Tyr
 435 440

<210> 2
 <211> 443
 <212> PRT
 <213> Human immunodeficiency virus

<400> 2

Met Gly Ala Arg Ala Ser Val Leu Ser Gly Gly Glu Leu Asp Lys Trp
 1 5 10 15

Glu Lys Ile Arg Leu Arg Pro Gly Gly Lys Lys Lys Tyr Lys Leu Lys
 20 25 30

His Ile Val Trp Ala Ser Arg Glu Leu Glu Arg Phe Ala Val Asn Pro
 35 40 45

Gly Leu Leu Glu Thr Ser Glu Gly Cys Arg Gln Ile Leu Gly Gln Leu
 50 55 60

Gln Pro Ser Leu Gln Thr Gly Ser Glu Glu Leu Arg Ser Leu Tyr Asn
 65 70 75 80

Thr Val Ala Thr Leu Tyr Cys Val His Gln Arg Ile Asp Val Lys Asp
85 90 95

Thr Lys Glu Ala Leu Glu Lys Ile Glu Glu Glu Gln Asn Lys Ser Lys
100 105 110

Lys Lys Ala Gln Gln Ala Ala Ala Ala Gly Thr Gly Asn Ser Ser
115 120 125

Gln Val Ser Gln Asn Tyr Pro Ile Val Gln Asn Leu Gln Gly Gln Met
130 135 140

Val His Gln Ala Ile Ser Pro Arg Thr Leu Asn Ala Trp Val Lys Val
145 150 155 160

Val Glu Glu Lys Ala Phe Ser Pro Glu Val Ile Pro Met Phe Ser Ala
165 170 175

Leu Ser Glu Gly Ala Thr Pro Gln Asp Leu Asn Thr Met Leu Asn Thr
180 185 190

Val Gly Gly His Gln Ala Ala Met Gln Met Leu Lys Glu Thr Ile Asn
195 200 205

Glu Glu Ala Ala Glu Trp Asp Arg Val His Pro Val His Ala Gly Pro
210 215 220

Ile Ala Pro Gly Gln Met Arg Glu Pro Arg Gly Ser Asp Ile Ala Gly
225 230 235 240

Thr Thr Ser Thr Leu Gln Glu Gln Ile Gly Trp Met Thr Asn Asn Pro
245 250 255

Pro Ile Pro Val Gly Glu Ile Tyr Lys Arg Trp Ile Ile Leu Gly Leu
260 265 270

Asn Lys Ile Val Arg Met Tyr Ser Pro Thr Ser Ile Leu Asp Ile Arg
275 280 285

Gln Gly Pro Lys Glu Pro Phe Arg Asp Tyr Val Asp Arg Phe Tyr Lys
290 295 300

Thr Leu Arg Ala Glu Gln Ala Ser Gln Asp Val Lys Asn Trp Met Thr

```
<220>
<221> CDS
<222> (1)..(3012)
<223>
```

<400> 3																
ttt	ttt	agg	gaa	gat	ctg	gcc	ttc	cta	caa	ggg	aag	gcc	agg	gaa	ttt	48
Phe	Phe	Arg	Glu	Asp	Leu	Ala	Phe	Leu	Gln	Gly	Lys	Ala	Arg	Glu	Phe	
1				5					10					15		
tct	tca	gag	cag	acc	aga	gcc	aac	agc	ccc	acc	aga	aga	gag	ctt	cag	96
Ser	Ser	Glu	Gln	Thr	Arg	Ala	Asn	Ser	Pro	Thr	Arg	Arg	Glu	Leu	Gln	
			20					25					30			
gtt	tg	gga	gga	gaa	aac	aac	tcc	ctc	tca	gaa	gca	gga	gcc	gat	aga	144
Val	Trp	Gly	Gly	Glu	Asn	Asn	Ser	Leu	Ser	Glu	Ala	Gly	Ala	Asp	Arg	

35	40	45	
caa gga act gta tcc ttt aac ttc cct cag atc act ctt tgg caa cga Gln Gly Thr Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg 50 55 60			192
ccc ctc gtc aca ata agg ata ggg ggg caa cta aag gaa gct cta tta Pro Leu Val Thr Ile Arg Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu 65 70 75 80			240
gat aca gga gca gat gat aca gta tta gaa gaa atg aat ttg cca gga Asp Thr Gly Ala Asp Asp Thr Val Leu Glu Glu Met Asn Leu Pro Gly 85 90 95			288
aaa tgg aaa cca aaa atg ata ggg gga att gga ggt ttt atc aaa gta Lys Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val 100 105 110			336
aga cag tac gat cag ata cct gta gaa atc tgt gga cat aaa gct ata Arg Gln Tyr Asp Gln Ile Pro Val Glu Ile Cys Gly His Lys Ala Ile 115 120 125			384
ggt aca gta tta gta gga cct aca cct gtc aac ata att gga aga aat Gly Thr Val Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn 130 135 140			432
ctg ttg act cag att ggt tgt act tta aat ttc ccc att agt cct att Leu Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe Pro Ile Ser Pro Ile 145 150 155 160			480
gaa act gta cca gta aaa tta aag cca gga atg gat ggc cca aaa gtt Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val 165 170 175			528
aag caa tgg cca ttg aca gaa gaa aaa ata aaa gca tta gta gag ata Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile 180 185 190			576
tgt aca gaa atg gaa aag gaa ggg aaa att tca aaa att ggg cct gaa Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu 195 200 205			624
aat cca tac aat act cca gta ttt gct ata aag aaa aaa gac agt act Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr 210 215 220			672
aaa tgg aga aaa cta gta gat ttc aga gaa ctt aat aaa aga act caa Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln 225 230 235 240			720
gac ttc tgg gaa gtt cag tta gga ata cca cac ccc gca ggg tta aaa Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys 245 250 255			768
aag aaa aaa tca gta aca gta ttg gat gtg ggt gat gca tac ttt tca Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser 260 265 270			816

gtt ccc tta gat aaa gac ttt aga aag tat act gca ttt acc ata cct Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro 275 280 285	864
agt ata aac aat gag aca cca ggg att aga tat cag tac aat gtg ctg Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu 290 295 300	912
cca cag gga tgg aaa gga tca cca gca ata ttc caa agt agc atg aca Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr 305 310 315 320	960
aaa atc tta gag cct ttt aga aaa cag aat cca gac ata gtt atc tat Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr 325 330 335	1008
caa tac atg gat gat ttg tat gta gga tct gac tta gaa ata ggg cag Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln 340 345 350	1056
cat aga aca aaa ata gag gaa ctg aga cag cat ctg ttg agg tgg gga His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly 355 360 365	1104
ttt acc aca cca gac aaa aaa cat cag aaa gaa cct cca ttc ctt tgg Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp 370 375 380	1152
atg ggt tat gaa ctc cat cct gat aaa tgg aca gta cag cct ata atg Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Met 385 390 395 400	1200
ctg cca gaa aaa gac agc tgg act gtc aat gac ata cag aag tta gtg Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val 405 410 415	1248
gga aaa ttg aat tgg gca agt cag att tat gca ggg att aaa gta aag Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys 420 425 430	1296
cag tta tgt aaa ctc ctt aga gga acc aaa gca cta aca gaa gta ata Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile 435 440 445	1344
cca cta aca gaa gaa gca gag cta gaa ctg gca gaa aac agg gag att Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile 450 455 460	1392
cta aaa gaa cca gta cat gaa gta tat tat gac cca tca aaa gac tta Leu Lys Glu Pro Val His Glu Val Tyr Tyr Asp Pro Ser Lys Asp Leu 465 470 475 480	1440
gta gca gaa ata cag aag cag ggg caa ggc caa tgg aca tat caa att Val Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile 485 490 495	1488

tat caa gag cca ttt aaa aat ctg aaa aca gga aag tat gca agg atg	1536
Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met	
500 505 510	
agg ggt gcc cac act aat gat gta aaa cag tta aca gag gca gtg caa	1584
Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln	
515 520 525	
aaa gta tcc aca gaa agc ata gta ata tgg gga aag att cct aaa ttt	1632
Lys Val Ser Thr Glu Ser Ile Val Ile Trp Gly Lys Ile Pro Lys Phe	
530 535 540	
aaa cta ccc ata caa aag gaa aca tgg gaa gca tgg tgg atg gag tat	1680
Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Ala Trp Trp Met Glu Tyr	
545 550 555 560	
tgg caa gct acc tgg att cct gag tgg gag ttt gtc aat acc cct ccc	1728
Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro	
565 570 575	
tta gtg aaa tta tgg tac cag tta gag aaa gaa ccc ata gta gga gca	1776
Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala	
580 585 590	
gaa act ttc tat gta gat ggg gca gct aat agg gag act aaa tta gga	1824
Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly	
595 600 605	
aaa gca gga tat gtt act gac aga gga aga caa aaa gtt gtc tcc ata	1872
Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val Ser Ile	
610 615 620	
gct gac aca aca aat cag aag act gaa tta caa gca att cat cta gct	1920
Ala Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile His Leu Ala	
625 630 635 640	
ttg cag gat tcg gga tta gaa gta aac ata gta aca gac tca caa tat	1968
Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr	
645 650 655	
gca tta gga atc att caa gca caa cca gat aag agt gaa tca gag tta	2016
Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu	
660 665 670	
gtc agt caa ata ata gag cag tta ata aaa aag gaa aag gtc tac ctg	2064
Val Ser Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu	
675 680 685	
gca tgg gta cca gca cac aaa gga att gga gga aat gaa caa gta gat	2112
Ala Trp Val Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp	
690 695 700	
aaa tta gtc agt gct gga atc agg aaa gta cta ttt ttg aat gga ata	2160
Lys Leu Val Ser Ala Gly Ile Arg Lys Val Leu Phe Leu Asn Gly Ile	
705 710 715 720	
gat aag gcc caa gaa gaa cat gag aaa tat cac agt aat tgg aga gca	2208

Asp	Lys	Ala	Gln	Glu	Glu	His	Glu	Lys	Tyr	His	Ser	Asn	Trp	Arg	Ala	
			725						730					735		
atg	gct	agt	gat	ttt	aac	ctg	cca	cct	gta	gta	gca	aaa	gaa	ata	gta	2256
Met	Ala	Ser	Asp	Phe	Asn	Leu	Pro	Pro	Val	Val	Ala	Lys	Glu	Ile	Val	
			740					745					750			
gcc	agc	tgt	gat	aaa	tgt	cag	cta	aaa	gga	gaa	gcc	atg	cat	gga	caa	2304
Ala	Ser	Cys	Asp	Lys	Cys	Gln	Leu	Lys	Gly	Glu	Ala	Met	His	Gly	Gln	
			755				760					765				
gta	gac	tgt	agt	cca	gga	ata	tgg	caa	cta	gat	tgt	aca	cat	cta	gaa	2352
Val	Asp	Cys	Ser	Pro	Gly	Ile	Trp	Gln	Leu	Asp	Cys	Thr	His	Leu	Glu	
	770					775					780					
gga	aaa	att	atc	ctg	gta	gca	gtt	cat	gta	gcc	agt	gga	tat	ata	gaa	2400
Gly	Lys	Ile	Ile	Leu	Val	Ala	Val	His	Val	Ala	Ser	Gly	Tyr	Ile	Glu	
	785				790					795					800	
gca	gaa	gtt	att	cca	gca	gag	aca	ggg	cag	gaa	aca	gca	tat	ttt	ctc	2448
Ala	Glu	Val	Ile	Pro	Ala	Glu	Thr	Gly	Gln	Glu	Thr	Ala	Tyr	Phe	Leu	
				805					810					815		
tta	aaa	tta	gca	gga	aga	tgg	cca	gta	aaa	aca	ata	cat	aca	gac	aat	2496
Leu	Lys	Leu	Ala	Gly	Arg	Trp	Pro	Val	Lys	Thr	Ile	His	Thr	Asp	Asn	
			820				825						830			
ggc	agc	aat	ttc	acc	agt	act	acg	gtt	aag	gcc	gcc	tgt	tgg	tgg	gca	2544
Gly	Ser	Asn	Phe	Thr	Ser	Thr	Thr	Val	Lys	Ala	Ala	Cys	Trp	Trp	Ala	
		835					840					845				
ggg	atc	aag	cag	gaa	ttt	ggc	att	ccc	tac	aat	ccc	caa	agt	caa	gga	2592
Gly	Ile	Lys	Gln	Glu	Phe	Gly	Ile	Pro	Tyr	Asn	Pro	Gln	Ser	Gln	Gly	
	850					855					860					
gta	gta	gaa	tct	atg	aat	aat	gaa	tta	aag	aaa	att	ata	gga	cag	gta	2640
Val	Val	Glu	Ser	Met	Asn	Asn	Glu	Leu	Lys	Lys	Ile	Ile	Gly	Gln	Val	
	865				870					875					880	
aga	gat	cag	gct	gaa	cac	ctt	aag	aca	gca	gta	caa	atg	gca	gta	ttc	2688
Arg	Asp	Gln	Ala	Glu	His	Leu	Lys	Thr	Ala	Val	Gln	Met	Ala	Val	Phe	
				885					890					895		
atc	cac	aat	ttt	aaa	aga	aaa	ggg	ggg	att	ggg	gga	tac	agt	gca	ggg	2736
Ile	His	Asn	Phe	Lys	Arg	Lys	Gly	Gly	Ile	Gly	Gly	Tyr	Ser	Ala	Gly	
			900				905						910			
gaa	aga	ata	gta	gac	ata	ata	gca	aca	gac	ata	caa	act	aaa	gaa	cta	2784
Glu	Arg	Ile	Val	Asp	Ile	Ile	Ala	Thr	Asp	Ile	Gln	Thr	Lys	Glu	Leu	
			915				920					925				
caa	aag	caa	att	aca	aaa	att	caa	aat	ttt	cgg	gtt	tat	tac	agg	gac	2832
Gln	Lys	Gln	Ile	Thr	Lys	Ile	Gln	Asn	Phe	Arg	Val	Tyr	Tyr	Arg	Asp	
			930			935					940					
aac	aaa	gat	ccc	ctt	tgg	aaa	gga	cca	gca	aag	ctt	ctc	tgg	aaa	ggt	2880
Asn	Lys	Asp	Pro	Leu	Trp	Lys	Gly	Pro	Ala	Lys	Leu	Leu	Trp	Lys	Gly	

10/23

945		950		955		960	
gaa ggg gca gta gta ata caa gat aat agt gac ata aaa gta gtg cca							2928
Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro							
	965			970		975	
aga aga aaa gca aaa atc att agg gat tat gga aaa cag atg gca ggt							2976
Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met Ala Gly							
	980			985		990	
gat gat tgt gtg gca agt aga cag gat gag gat tag							3012
Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp							
	995			1000			

<210> 4
 <211> 1003
 <212> PRT
 <213> Human immunodeficiency virus

<400> 4

Phe Phe Arg Glu Asp Leu Ala Phe Leu Gln Gly Lys Ala Arg Glu Phe							
1	5			10			15
Ser Ser Glu Gln Thr Arg Ala Asn Ser Pro Thr Arg Arg Glu Leu Gln							
	20			25			30
Val Trp Gly Gly Glu Asn Asn Ser Leu Ser Glu Ala Gly Ala Asp Arg							
	35			40			45
Gln Gly Thr Val Ser Phe Asn Phe Pro Gln Ile Thr Leu Trp Gln Arg							
	50			55			60
Pro Leu Val Thr Ile Arg Ile Gly Gly Gln Leu Lys Glu Ala Leu Leu							
	65			70			75
Asp Thr Gly Ala Asp Asp Thr Val Leu Glu Glu Met Asn Leu Pro Gly							
	85			90			95
Lys Trp Lys Pro Lys Met Ile Gly Gly Ile Gly Gly Phe Ile Lys Val							
	100			105			110
Arg Gln Tyr Asp Gln Ile Pro Val Glu Ile Cys Gly His Lys Ala Ile							
	115			120			125
Gly Thr Val Leu Val Gly Pro Thr Pro Val Asn Ile Ile Gly Arg Asn							
	130			135			140

Leu Leu Thr Gln Ile Gly Cys Thr Leu Asn Phe Pro Ile Ser Pro Ile
 145 150 155 160

Glu Thr Val Pro Val Lys Leu Lys Pro Gly Met Asp Gly Pro Lys Val
 165 170 175

Lys Gln Trp Pro Leu Thr Glu Glu Lys Ile Lys Ala Leu Val Glu Ile
 180 185 190

Cys Thr Glu Met Glu Lys Glu Gly Lys Ile Ser Lys Ile Gly Pro Glu
 195 200 205

Asn Pro Tyr Asn Thr Pro Val Phe Ala Ile Lys Lys Lys Asp Ser Thr
 210 215 220

Lys Trp Arg Lys Leu Val Asp Phe Arg Glu Leu Asn Lys Arg Thr Gln
 225 230 235 240

Asp Phe Trp Glu Val Gln Leu Gly Ile Pro His Pro Ala Gly Leu Lys
 245 250 255

Lys Lys Lys Ser Val Thr Val Leu Asp Val Gly Asp Ala Tyr Phe Ser
 260 265 270

Val Pro Leu Asp Lys Asp Phe Arg Lys Tyr Thr Ala Phe Thr Ile Pro
 275 280 285

Ser Ile Asn Asn Glu Thr Pro Gly Ile Arg Tyr Gln Tyr Asn Val Leu
 290 295 300

Pro Gln Gly Trp Lys Gly Ser Pro Ala Ile Phe Gln Ser Ser Met Thr
 305 310 315 320

Lys Ile Leu Glu Pro Phe Arg Lys Gln Asn Pro Asp Ile Val Ile Tyr
 325 330 335

Gln Tyr Met Asp Asp Leu Tyr Val Gly Ser Asp Leu Glu Ile Gly Gln
 340 345 350

His Arg Thr Lys Ile Glu Glu Leu Arg Gln His Leu Leu Arg Trp Gly
 355 360 365

12/23

Phe Thr Thr Pro Asp Lys Lys His Gln Lys Glu Pro Pro Phe Leu Trp
 370 375 380

Met Gly Tyr Glu Leu His Pro Asp Lys Trp Thr Val Gln Pro Ile Met
 385 390 395 400

Leu Pro Glu Lys Asp Ser Trp Thr Val Asn Asp Ile Gln Lys Leu Val
 405 410 415

Gly Lys Leu Asn Trp Ala Ser Gln Ile Tyr Ala Gly Ile Lys Val Lys
 420 425 430

Gln Leu Cys Lys Leu Leu Arg Gly Thr Lys Ala Leu Thr Glu Val Ile
 435 440 445

Pro Leu Thr Glu Glu Ala Glu Leu Glu Leu Ala Glu Asn Arg Glu Ile
 450 455 460

Leu Lys Glu Pro Val His Glu Val Tyr Tyr Asp Pro Ser Lys Asp Leu
 465 470 475 480

Val Ala Glu Ile Gln Lys Gln Gly Gln Gly Gln Trp Thr Tyr Gln Ile
 485 490 495

Tyr Gln Glu Pro Phe Lys Asn Leu Lys Thr Gly Lys Tyr Ala Arg Met
 500 505 510

Arg Gly Ala His Thr Asn Asp Val Lys Gln Leu Thr Glu Ala Val Gln
 515 520 525

Lys Val Ser Thr Glu Ser Ile Val Ile Trp Gly Lys Ile Pro Lys Phe
 530 535 540

Lys Leu Pro Ile Gln Lys Glu Thr Trp Glu Ala Trp Trp Met Glu Tyr
 545 550 555 560

Trp Gln Ala Thr Trp Ile Pro Glu Trp Glu Phe Val Asn Thr Pro Pro
 565 570 575

Leu Val Lys Leu Trp Tyr Gln Leu Glu Lys Glu Pro Ile Val Gly Ala
 580 585 590

Glu Thr Phe Tyr Val Asp Gly Ala Ala Asn Arg Glu Thr Lys Leu Gly
 595 600 605

Lys Ala Gly Tyr Val Thr Asp Arg Gly Arg Gln Lys Val Val Ser Ile
 610 615 620

Ala Asp Thr Thr Asn Gln Lys Thr Glu Leu Gln Ala Ile His Leu Ala
 625 630 635 640

Leu Gln Asp Ser Gly Leu Glu Val Asn Ile Val Thr Asp Ser Gln Tyr
 645 650 655

Ala Leu Gly Ile Ile Gln Ala Gln Pro Asp Lys Ser Glu Ser Glu Leu
 660 665 670

Val Ser Gln Ile Ile Glu Gln Leu Ile Lys Lys Glu Lys Val Tyr Leu
 675 680 685

Ala Trp Val Pro Ala His Lys Gly Ile Gly Gly Asn Glu Gln Val Asp
 690 695 700

Lys Leu Val Ser Ala Gly Ile Arg Lys Val Leu Phe Leu Asn Gly Ile
 705 710 715 720

Asp Lys Ala Gln Glu Glu His Glu Lys Tyr His Ser Asn Trp Arg Ala
 725 730 735

Met Ala Ser Asp Phe Asn Leu Pro Pro Val Val Ala Lys Glu Ile Val
 740 745 750

Ala Ser Cys Asp Lys Cys Gln Leu Lys Gly Glu Ala Met His Gly Gln
 755 760 765

Val Asp Cys Ser Pro Gly Ile Trp Gln Leu Asp Cys Thr His Leu Glu
 770 775 780

Gly Lys Ile Ile Leu Val Ala Val His Val Ala Ser Gly Tyr Ile Glu
 785 790 795 800

Ala Glu Val Ile Pro Ala Glu Thr Gly Gln Glu Thr Ala Tyr Phe Leu
 805 810 815

Leu Lys Leu Ala Gly Arg Trp Pro Val Lys Thr Ile His Thr Asp Asn

14/23

820	825	830
Gly Ser Asn Phe Thr Ser Thr Thr Val Lys Ala Ala Cys Trp Trp Ala		
835	840	845
Gly Ile Lys Gln Glu Phe Gly Ile Pro Tyr Asn Pro Gln Ser Gln Gly		
850	855	860
Val Val Glu Ser Met Asn Asn Glu Leu Lys Lys Ile Ile Gly Gln Val		
865	870	875
Arg Asp Gln Ala Glu His Leu Lys Thr Ala Val Gln Met Ala Val Phe		
885	890	895
Ile His Asn Phe Lys Arg Lys Gly Gly Ile Gly Gly Tyr Ser Ala Gly		
900	905	910
Glu Arg Ile Val Asp Ile Ile Ala Thr Asp Ile Gln Thr Lys Glu Leu		
915	920	925
Gln Lys Gln Ile Thr Lys Ile Gln Asn Phe Arg Val Tyr Tyr Arg Asp		
930	935	940
Asn Lys Asp Pro Leu Trp Lys Gly Pro Ala Lys Leu Leu Trp Lys Gly		
945	950	955
Glu Gly Ala Val Val Ile Gln Asp Asn Ser Asp Ile Lys Val Val Pro		
965	970	975
Arg Arg Lys Ala Lys Ile Ile Arg Asp Tyr Gly Lys Gln Met Ala Gly		
980	985	990
Asp Asp Cys Val Ala Ser Arg Gln Asp Glu Asp		
995	1000	

<210> 5
 <211> 501
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(501)
 <223>

<400> 5
 atg aaa tat aca agt tat atc ttg gct ttt cag ctc tgc atc gtt ttg 48
 Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

ggt tct ctt ggc tgt tac tgc cag gac cca tat gta aaa gaa gca gaa 96
 Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
 20 25 30

aac ctt aag aaa tat ttt aat gca ggt cat tca gat gta gcg gat aat 144
 Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
 35 40 45

gga act ctt ttc tta ggc att ttg aag aat tgg aaa gag gag agt gac 192
 Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
 50 55 60

aga aaa ata atg cag agc caa att gtc tcc ttt tac ttc aaa ctt ttt 240
 Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
 65 70 75 80

aaa aac ttt aaa gat gac cag agc atc caa aag agt gtg gag acc atc 288
 Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
 85 90 95

aag gaa gac atg aat gtc aag ttt ttc aat agc aac aaa aag aaa cga 336
 Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
 100 105 110

gat gac ttc gaa aag ctg act aat tat tgc gta act gac ttg aat gtc 384
 Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
 115 120 125

caa cgc aaa gca ata cat gaa ctc atc caa gtg atg gct gaa ctg tgc 432
 Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
 130 135 140

cca gca gct aaa aca ggg aag cga aaa agg agt cag atg ctg ttt cga 480
 Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
 145 150 155 160

ggt cga aga gca tcc cag taa 501
 Gly Arg Arg Ala Ser Gln
 165

<210> 6
 <211> 166
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Lys Tyr Thr Ser Tyr Ile Leu Ala Phe Gln Leu Cys Ile Val Leu
 1 5 10 15

Gly Ser Leu Gly Cys Tyr Cys Gln Asp Pro Tyr Val Lys Glu Ala Glu
20 25 30

Asn Leu Lys Lys Tyr Phe Asn Ala Gly His Ser Asp Val Ala Asp Asn
35 40 45

Gly Thr Leu Phe Leu Gly Ile Leu Lys Asn Trp Lys Glu Glu Ser Asp
50 55 60

Arg Lys Ile Met Gln Ser Gln Ile Val Ser Phe Tyr Phe Lys Leu Phe
65 70 75 80

Lys Asn Phe Lys Asp Asp Gln Ser Ile Gln Lys Ser Val Glu Thr Ile
85 90 95

Lys Glu Asp Met Asn Val Lys Phe Phe Asn Ser Asn Lys Lys Lys Arg
100 105 110

Asp Asp Phe Glu Lys Leu Thr Asn Tyr Ser Val Thr Asp Leu Asn Val
115 120 125

Gln Arg Lys Ala Ile His Glu Leu Ile Gln Val Met Ala Glu Leu Ser
130 135 140

Pro Ala Ala Lys Thr Gly Lys Arg Lys Arg Ser Gln Met Leu Phe Arg
145 150 155 160

Gly Arg Arg Ala Ser Gln
165

<210> 7

<211> 11333

<212> DNA

<213> recombinant vector

<400> 7

agacagttat cccaatacgg tatacaagga gacaatttat caatttttgt agattcttcc 60

aatgaagttg ctataaacag gcaactctatt ataggagcta gacagttgaa tcctatatgc 120

gtagtatctt ttatatccctt tgatccagaa cataaagttt ttttcgttat atatgttggt 180

agatataaag ataagtattg tggaatttcc tacgtagctg atagagaaga tatgtacaaa 240

gttatcaaca ggatataccc gtacgttagt tgtttttacc tcgtatcaga tggtataata 300

aattttcata ctactcccggt agctaatacac actagaaata ttaaaccctt tccagttaat	360
tattgtaata ctttatgtga aatagtatat gattttgaat atttaaagtt tgaacaaggt	420
gttatgtcta ttccgggtgtt catgcctttt gtacaaaaac agtttgtatc tattatcaat	480
ttaccagatg atattctcat aacatgtaca gcgtccagta acatagaata cataacacat	540
atagataata aaaagctaaa aagaatactt ataataataa aagataaatt tctaaagggt	600
actatcatgc aagggtacttt taaaaaagta aatatcataa gacacaagaa gtatacatat	660
actataacgt attcttcttt tgattgccct aaactagaag atactaagtc atcgctgcca	720
agtacgtgca ataaagccat attagatggg cgtagatatg ttacaaaaac ttttaatgat	780
acaatataaa tggaaatagc tagagaaacg ctaataacga taggccttac tatattagta	840
gtgttattga taataactgg attctcgcta gtgctaagat taataccggg tgtttatagt	900
tcagtatcga ggtcatcatt tacagcagga agaatacttc gttttatgga aatattttct	960
actattatgt ttattcctgg aataattata ttgtacgctg cttatataag aaaaattaaa	1020
atgaaaaata attagaatct gaaaatgtct tctggaagca tccatgttat tacaggccct	1080
atgttttccg gtaaaacatc ggagctagta agaagaataa aaagatttat gctatctaac	1140
tttaaagtga ttattattaa acattgtgga gataatagat ataatgagga tgatataaac	1200
aaagtatata ctcatgatct attgtttatg gaggctacgg catottctaa tctatctgta	1260
ttagtaccta cgctattaaa tgatggagtt caggtaatag gtatagacga ggctcaattc	1320
tttctagaca tagtagaatt tagtgaatcc atggctaatt taggtaaaac agttattgtg	1380
gccgcgctta acggtgattt taaacgcgaa ttattcggtg acgtatataa gttattatca	1440
ttagctgaaa cagtgtccag ttgacagct atttgcggtg aatgctattg cgacgcttcg	1500
ttttctaaac gagttacaga aaataaagaa gtaatggata taggtggtaa agataaatac	1560
atagccgtgt gtaggaaatg tttttttagt aattaagggg agatctcccc atggcccaaa	1620
gcgggggttg aacagggttt cgctcagggt tgcctgtgtc atggatgcag cctccagaat	1680
acttactgga aactattgta acccgctga agttaaaaag aacaacgccc ggagtgcca	1740
ggcgttgaaa agattagcga ccggagattg gcgggacgaa tacgacgccc atatcccacg	1800
gctgttcaat ccaggatatc tgcgggatat caacaacata gtcacacacc agcggacgac	1860
cagccgggtt tgccaagatg gtgacaaagt gcgcttttgg atacatttca cgaatcgcaa	1920
ccgcagtacc accggtatcc accagggtcat caataacgat gaagccttcg ccatcgctt	1980

ctgcgcgttt cagcacttta agctcgcgct ggttgtcgtg atcgtagctg gaaatacaaa 2040
cggatcgcac atgacgaata ccagttcac gcgccagtaa cgcacccggg accagaccgc 2100
cacggcttac ggcaataatg cctttccatt gttcagaagg catcagtcgg cttgcgagtt 2160
tacgtgcatg gatctgcaac atgtcccagg tgacgatgta tttttcgctc atgtgaagtg 2220
tcccagcctg tttatctacg gcttaaaaag tgttcgaggg gaaaatagggt tgcgcgagat 2280
tatagagatc cgtcactggt ctttatgatc tacttcctta ccgtgcaata aattagaata 2340
tattttctac ttttacgaga aattaattat tgtatttatt atttatgggt gaaaaactta 2400
ctataaaaag cgggtgggtt tggaattagt gatcagttta tgtatatcgc aactaccggc 2460
atatggctat tcgacatcga gaacattacc cacatgataa gagattgtat cagtttcgta 2520
gtcttgagta ttggtattac tatatagtat atgtcgggaa ttcagatcca tgcagatccc 2580
ccctgccogg ttattattat ttttgacacc agaccaactg gtaatggtag cgaccggcgc 2640
tcagctggaa ttccgccgat actgacgggc tccaggagtc gtgccacca atccccatat 2700
ggaaaccgtc gatattcagc catgtgcctt cttccgcgtg cagcagatgg cgatggctgg 2760
tttccatcag ttgctgttga ctgtagcggc tgatgttgaa ctggaagtcg ccgcgccact 2820
gggtggtggc ataattcaat tcgcgcgtcc cgcagcgcag accgttttcg ctcggaaga 2880
cgtacggggg atacatgtct gacaatggca gatcccagcg gtcaaaacag gcggcagtaa 2940
ggcggtcggg atagttttct tgccggccta atccgagcca gtttaccgc tctgctacct 3000
gcgccagctg gcagttcagg ccaatccgcg ccggatgcgg tgtatcgctc gccacttcaa 3060
catcaacggt aatcgccatt tgaccactac catcaatccg gtaggttttc cggctgataa 3120
ataaggtttt cccctgatgc tgccacgcgt gagcggtcgt aatcagcacc gcatcagcaa 3180
gtgtatctgc cgtgcactgc aacaacgctg cttcggcctg gtaatggccc gccgccttcc 3240
agcgttcgac ccaggcggtta gggcgaatgc gggtcgcttc acttacgcca atgtcgttat 3300
ccagcgggtg acgggtgaac tgatcgcgca gcggcgtcag cagttgtttt ttatcgccaa 3360
tccacatctg tgaaagaaaag cctgactggc ggttaaattg ccaacgctta ttaccagct 3420
cgatgcaaaa atccatttcg ctggtggtca gatgcgggat ggcgtgggac gcggcgggga 3480
gcgtcacact gaggttttcc gccagacgcc actgctgcca ggcgctgatg tgcccggtt 3540
ctgaccatgc ggtcgcgttc ggttgcaacta cgcgtactgt gagccagagt tgcccggcgc 3600
tctccggctg cggtagttca ggcagttcaa tcaactgttt acctgtgga gcgacatcca 3660
gaggcacttc accgcttgcc agcggcttac catccagcgc caccatccag tgcaggagct 3720

cgttatcgct atgacggaac aggtattcgc tggtcacttc gatgggtttgc ccggataaac 3780
ggaactggaa aaactgctgc tgggtgttttg cttccgctcag cgctggatgc ggcgtgcggt 3840
cggcaaagac cagaccgttc atacagaact ggcgatcggt cggcgtatcg ccaaaatcac 3900
cgccgtaagc cgaccacggg ttgccgtttt catcatattt aatcagcgcac tgatccaccc 3960
agtcccagac gaagccgccc tgtaaacggg gatactgacg aaacgcctgc cagtatttag 4020
cgaaaccgcc aagactgtta cccatcgctt gggcgtattc gcaaaggatc agcgggcgcg 4080
tctctccagg tagcgaaagc ctttttttga tggaccattt cggcacagcc ggggaagggct 4140
ggtcttcac cagcgcgcgcg tacatcgggc aaataatatc ggtggccgtg gtgtcggctc 4200
cgccgccttc atactgcacc gggcggaag gatcgacaga tttgatccag cgatacagcg 4260
cgctcgtgatt agcgcctggg cctgattcat tccccagcga ccagatgatc aactcgggt 4320
gattacgatc gcgctgcacc attcgcgtta cgcgttcgct catcgccggt agccagcgcg 4380
gatcatcggc cagacgattc attggcacca tgccgtgggt ttcaatattg gcttcatcca 4440
ccacatacag gccgtagcgg tcgcacagcg tgtaccacag cggatgggtc ggataatgcg 4500
aacagcgcac ggcgttaaag ttgttctgct tcatcagcag gatatcctgc accatcgtct 4560
gctcatccat gacctgacca tgcagaggat gatgctcgtg acggttaacg cctcgaatca 4620
gcaacggctt gccgttcagc agcagcagac ctttttcaat ccgcacctcg cggaaaccga 4680
catcgcaggc ttctgcttca atcagcgtgc cgctggcggt gtgcagttca accaccgcac 4740
gatagagatt cgggatttcg gcgctccaca gtttcgggtt ttgcagcttc agacgtagt 4800
tgacgcgatc ggcataacca ccacgctcat cgataatttc accgcgaaa ggcgcggtgc 4860
cgctggcgac ctgcgtttca ccctgccata aagaaactgt taccgtagg tagtcacgca 4920
actcgcgcga catctgaact tcagcctcca gtacagcgcg gctgaaatca tcattaaagc 4980
gagtggcaac atggaaatcg ctgatttgtg tagtcgggtt atgcagcaac gagacgtcac 5040
ggaaaatgcc gctcatccgc cacatatcct gatcttcag ataactgccg tcaactccaac 5100
gcagcaccat caccgcgagg cggttttctc cggcgcgtaa aaatgcgctc aggtcaaatt 5160
cagacggcaa acgactgtcc tggccgtaac cgaccacgcg cccgttgac cacagatgaa 5220
acgccgagtt aacgccatca aaaataattc gogtctggcc ttctgttagc cagctttcat 5280
caacattaaa tgtgagcgag taacaaccgc toggattctc cgtgggaaca aacggcggt 5340
tgaccgtaat gggataggtt acgttggtgt agatgggcgc atcgtaaccg tgcactgcc 5400

agtttgaggg gacgacgaca gtatcggcct caggaagatc gcactccagc cagctttccg 5460
gcaccgcttc tgggtgccgga aaccaggcaa agcgccattc gccattcagg ctgcgcaact 5520
gttggaagg gcgatcgggtg cgggcctctt cgctattacg ccagctggcg aaagggggat 5580
gtgctgcaag gcgattaagt tgggtaacgc cagggttttc ccagtcacga cgttgtaaaa 5640
cgacgggatc tagcatggat ctagccattt agtatcctaa aattgaattg taattatoga 5700
taataaatgg acggatcgat gaaatataca agttatatct tggcttttca gctctgcatc 5760
gttttggtt ctcttggtg ttactgccag gaccatattg taaaagaagc agaaaacctt 5820
aagaaatatt ttaatgcagg tcattcagat gtagcggata atggaactct tttcttaggc 5880
attttgaaga attggaaga ggagagtgc agaaaaataa tgcagagcca aattgtctcc 5940
ttttacttca aactttttta aaacttttaa gatgaccaga gcatccaaaa gagtgtggag 6000
accatcaagg aagacatgaa tgtcaagttt ttcaatagca acaaaaagaa acgagatgac 6060
ttcgaaaagc tgactaatta ttcggtaact gacttgaatg tccaacgcaa agcaatacat 6120
gaactcatcc aagtgatggc tgaactgtcg ccagcagcta aaacaggga gcgaaaaagg 6180
agtcagatgc tgtttcgagg tcgaagagca tcccagtaat ggttgcctg cctgcaatat 6240
ttgaatttta aatctaaatc tatttattaa tatttaacat tatttatatg gggaatatat 6300
ttttagactc atcaatcaaa taagtattta taatagcaac ttttttgtaa tggatcccag 6360
ctctctcgac gcaggactcg gcttgctgaa gcgcgcacag caagaggcga ggggcggcga 6420
ctggtgagta cgccaatttt tgactagcgg aggctagaag gagagagaga tgggtgcgag 6480
agcgtcggta ttaagcggg gagaattaga taaatggga aaaattcggg taaggccagg 6540
gggaaagaaa aaatataagt taaaacatat agtatgggca agcagggagc tagaacgatt 6600
cgcagtcaat cctggcctgt tagaaacatc agaaggctgc agacaaatat tgggacagct 6660
acagccatcc cttcagacag gatcagaaga acttagatca ttatataata cagtagcaac 6720
cctctattgt gtacatcaaa ggatagatgt aaaagacacc aaggaagctt tagagaagat 6780
agaggaagag caaaacaaaa gtaagaaaaa ggcacagcaa gcagcagctg cagctggcac 6840
aggaaacagc agccaggta gccaaaatta ccctatagtg cagaacctac aggggcaa 6900
ggtacatcag gccatatcac ctagaacttt aatgcatgg gtaaaagtag tagaagaaaa 6960
ggctttcagc ccagaagtaa taccatggtt ttcagcatta tcagaaggag ccacccaca 7020
agatttaaac accatgctaa acacagtggg gggacatcaa gcagccatgc aatgtttaa 7080
agagactatc aatgaggaag ctgcagaatg ggatagagtg catccagtgc atgcagggcc 7140

tattgcacca ggccaaatga gagaaccaag gggaagtgc atagcaggaa ctactagtac 7200
ccttcaggaa caaataggat ggatgacaaa taatccacct atcccagtag gagaaatcta 7260
taaaagatgg ataatcctgg gattaaataa aatagtaaga atgtatagcc ctaccagcat 7320
tctggacata agacaaggac caaaggaacc ctttagagat tatgtagacc ggttctataa 7380
aactctaaga gccgaacaag cttcacagga tgtaaaaaat tggatgacag aaaccttggt 7440
ggtccaaaat gcaaaccag attgtaagac ttttttaaaa gcattgggac cagcagctac 7500
actagaagaa atgatgacag catgtcaggg agtgggggga cccggccata aagcaagagt 7560
tttggtgaa gccatgagcc aagtaacaaa tccagctaac ataatgatgc agagaggcaa 7620
tttttaggaac caaagaaaga ctgttaagtg tttcaattgt ggcaaagaag ggcacatagc 7680
caaaaattgc agggccccta ggaaaaagg ctgttgagga tgtggaagg aaggacacca 7740
aatgaaagat tgcactgaga gacaggctaa ttttttaggg aagatctggc cttcctacaa 7800
gggaaggcca gggaattttc ttcagagcag accagagcca acagccccac cagaagagag 7860
cttcaggttt ggggaggaga aaacaactcc ctctcagaag caggagccga tagacaagga 7920
actgtatcct ttaacttccc tcagatcact ctttggcaac gaccctcgt cacaataagg 7980
ataggggggc aactaaagga agctctatta gatacaggag cagatgatac agtattagaa 8040
gaaatgaatt tgccaggaaa atggaaacca aaaatgatag ggggaattgg aggttttctc 8100
aaagtaagac agtacgatca gatacctgta gaaatctgtg gacataaagc tataggtaca 8160
gtattagtag gacctacacc tgtcaacata attggaagaa atctgttgac tcagattggt 8220
tgtactttaa atttccccat tagtcctatt gaaactgtac cagtaaaatt aaagccagga 8280
atggatggcc caaaagttaa gcaatggcca ttgacagaag aaaaaataaa agcattagta 8340
gagatatgta cagaaatgga aaaggaaggg aaaatttcaa aaattgggccc tgaaaatcca 8400
tacaatactc cagtatttgc tataaagaaa aaagacagta ctaaattggag aaaactagta 8460
gatttcagag aacttaataa aagaactcaa gacttctggg aagttcagtt aggaatacca 8520
caccgccgag ggttaaaaaa gaaaaaatca gtaacagtat tggatgtggg tgatgcatac 8580
ttttcagttc ccttagataa agactttaga aagtatactg catttaccat acctagtata 8640
aacaatgaga caccagggat tagatatcag tacaatgtgc tgccacaggg atggaaagga 8700
tcaccagcaa tattccaaag tagcatgaca aaaatcttag agccttttag aaaacagaat 8760
ccagacatag ttatctatca atacatggat gatttgtatg taggatctga cttagaaata 8820

gggcagcata gaacaaaaat agaggaactg agacagcatc tgttgaggtg gggatttacc 8880
acaccagaca aaaaacatca gaaagaacct ccattccttt ggatgggtta tgaactccat 8940
cctgataaat ggacagtaca gcctataatg ctgccagaaa aagacagctg gactgtcaat 9000
gacatacaga agttagtggg aaaattgaat tgggcaagtc agatttatgc agggattaaa 9060
gtaaagcagt tatgtaaact ccttagagga accaaagcac taacagaagt aataccacta 9120
acagaagaag cagagctaga actggcagaa aacagggaga ttctaaaaga accagtacat 9180
gaagtatatt atgaccatc aaaagactta gtagcagaaa tacagaagca ggggcaaggc 9240
caatggacat atcaaattta tcaagagcca tttaaaaatc tgaaaacagg aaagtatgca 9300
aggatgaggg gtgcccacac taatgatgta aaacagttaa cagaggcagt gcaaaaagta 9360
tccacagaaa gcatagtaat atggggaaag attcctaaat ttaaactacc catacaaaag 9420
gaaacatggg aagcatggtg gatggagtat tggcaagcta cctggattcc tgagtgggag 9480
tttgtcaata cccctccctt agtgaaatta tggtagcagt tagagaaaga acccatagta 9540
ggagcagaaa ctttctatgt agatggggca gctaataagg agactaaatt aggaaaagca 9600
ggatatgtta ctgacagagg aagacaaaaa gttgtotcca tagctgacac aacaaatcag 9660
aagactgaat tacaagcaat tcatctagct ttgcaggatt cgggattaga agtaaacata 9720
gtaacagact cacaatatgc attaggaatc attcaagcac aaccagataa gagtgaatca 9780
gagttagtca gtcaaataat agagcagtta ataaaaaagg aaaaggctca cctggcatgg 9840
gtaccagcac acaaaggaat tggaggaaat gaacaagtag ataaattagt cagtgtctgga 9900
atcaggaaag tactattttt gaatggaata gataaggccc aagaagaaca tgagaaatat 9960
cacagtaatt ggagagcaat ggctagtgat tttaacctgc cacctgtagt agcaaaaagaa 10020
atagtagcca gctgtgataa atgtcagcta aaaggagaag ccatgcatgg acaagtagac 10080
tgtagtccag gaatatggca actagattgt acacatctag aaggaaaaat taccctggta 10140
gcagttcatg tagccagtgg atatatagaa gcagaagtta ttccagcaga gacagggcag 10200
gaaacagcat attttctctt aaaattagca ggaagatggc cagtaaaaac aatacataca 10260
gacaatggca gcaatttcac cagtactacg gttaaggccg cctgttggtg ggcagggatc 10320
aagcaggaat ttggcattcc ctacaatccc caaagtcaag gagtagtaga atctatgaat 10380
aatgaattaa agaaaattat aggacaggta agagatcagg ctgaacacct taagacagca 10440
gtacaaatgg cagtattcat ccacaatttt aaaagaaaag gggggattgg gggatacagt 10500
gcaggggaaa gaatagtaga cataatagca acagacatac aaactaaaga actacaaaag 10560

caaattacaa aaattcaaaa ttttcgggtt tattacaggg acaacaaaga tcccctttgg 10620
aaaggaccag caaagcttct ctggaaaggt gaaggggcag tagtaataca agataatagt 10680
gacataaaaag tagtgccaag aagaaaagca aaaatcatta gggattatgg aaaacagatg 10740
gcagggtgatg attgtgtggc aagtagacag gatgaggatt agaacatgga aaagtttagt 10800
aaaacaccat agggtcgact gcagaagctt ccatggggag ctcttttagtg taataaattt 10860
aataaaatat tgacaaaata gttaaatgaa tatatgaaag tacattatac acggaatgga 10920
gttcgatatt agttcttgca gaatgatata ttctgttctc gaacaatata actttgttac 10980
tgataatcgt tataacaacc ataatcaaaa atttagaatt atattatact gtttaaaaga 11040
ttctacgata aagaaatata cgtacagggt tgttttctgaa attcactttg taagatacat 11100
aattaacaaa ttcaggggga aaaatcttta caaaattagt atagaagcta tagatatata 11160
aaaaggtaga caacaaataa tcagaacctt atttttttat caaaaaatta aaatataaat 11220
aaaatgaaaa ataacttgta tgaagaaaaa atgaacatga gtaagaaaca agtaaaaaact 11280
caaagtaaat gtaataataa cgcactctaga ttacatgcc tggatgcggt gca 11333